

Fig. 1



ICTB : 471	TGTCAGTGTCTACGGCCTCAACCAATGGATCTACGGCGTTGAAGAGCTGGCGACTTGGGT	530
SLR : 483	GGTGGGAGTTACGGTCTCGGACAAACAGGTGGACGGGTAGAACAGTTAGCCACTTGGAA	542
ICTB : 531	GGATCGCAACTCGGTTGCCGACTTCACCTCACGGGTTTACAGCTATCTGGGCAACCCCAA	590
SLR : 543	TGACCCACCTCTACCTTGCGCCAGGCCACTAGGGTATATAGCTTTTTAGGTAATCCCAA	602
ICTB : 591	CCTGCTGGCTGCTTATCTGGTGCCGACGACTGCCCTTTT-CTGCAGCAGCATCGGGGTGT	649
SLR : 603	TCTCTTGGCGGCTTACCTGTGTGCCCATGACGGGTTTGAGCTTGAGT-GCCCTGGTGGTAT	661
ICTB : 650	GGCGCGGCTGGCTCCCCAAGCTGCTGGCGATCG-CTGCGACAGTGCAGCAGCTTATGT	708
SLR : 662	GGCGACGGTGTGTGCCCAAACTGCTGG-GAGCAACCATGGTGATTGTTAACCTACTCTGT	720
ICTB : 709	CTGATCCTCACCTACAGTCGCGGTGGCTGGCTGGGTTTGTGCGCCATGATTTTGTCTGG	768
SLR : 721	CTCTTTTACCCAGAGCCGGGCGGTTGGCTAGCAGTGTGCCCCCTGGGAGCTACCTTC	780
ICTB : 769	GCGTTATTAGGGCTCTACTGGTTTCAACCCCGTCTACCCGACCCCTGGCGACGCTGGCTA	828
SLR : 781	CTGGCCCTTTGTTACTTCTGGTGGTTACCCCAATTACCCAAATTTTGGCAACGGTGTCT	840
ICTB : 829	TTCCCAAGTCGTATTGGGTGGACTAGTCGCGGTGCTCTT-GGTGGCGGTGCTTGGACT---	884
SLR : 841	TTGCCCCCTGGC---GATCGCC--GTGGCGGTTATATTAGGTGGGGGAGCGTTGATTGCG	894
ICTB : 885	-TG-AGCCGTTGCGGTGCGGTGTTGAGCATCTTGTGGGGCGTGAAGACAGCAGCAAC	942
SLR : 895	GTGGAACCGATTTCGACTCAGGGCCATGAGCATTTTGTGCTGGCGGGAAGACAGCAGTAAT	954

Fig. 2  
(Continued)



# Fig. 3

+++W++L F + PQ+WG S LHRL G ++W +S L EALG L+A+++ +APF  
 SLR : 5 ISIWRSLMFGGSPQEWGRGSLHRLVWGWSIQASVLWPHFEALGTALVAIIFIAAPF 64  
  
 ICTB : 61 VFSSALGLGLAAIAAYWALLSLTDIDLRQATPIHVLVLLYWGVDALATGLSPVRAALVG 120  
 ++ LG+ + A+WALL+ D + TPIH LV YW + A+A G SPV+ AA G  
 SLR : 65 TSTTMLGIFMLLCCGAFWALLTFADQPGKGLTPIHVLVFAWNCISAIWGFSPVKMAAASG 124  
  
 ICTB : 121 LAKLTLYLLVFALAAARVLRNPRLSLLFSVVVITSLFVSVYGLNQWIYGVVEELATWVDNR 180  
 LAKLT L +F LAAR+L+N + + L +VV++ L V YGL Q + GVE+LATW D  
 SLR : 125 LAKLTANLCLFLLAARLLONKQWLNRLVTVLLVGLLVGSYGLRQQVDGVEQLATWNDPT 184  
  
 ICTB : 181 SVADFTSRVYSYLGPNPDLAAYLVPTTAFSAAGVWGRWLPKLLAIAATGASSLCLILT 240  
 S +RVYS+LGPNPDLAAYLP T S +A+ VWR W PKLL + LCL T  
 SLR : 185 STLAQATRVSFLGNPNLDAAYLVPMTGSLSLVWVRRWPKLLGATMVIVNLLCLFFT 244  
  
 ICTB : 241 YSRGGWLGFBAMIFVWALLGLYWFQPRLPAPWRRWLFPPVVLGCLVAVLLVAVLGLLEPLRV 300  
 SRGGWL +A+ + L +W+ P+LP W+RW P+ + V + A++ +EP+R+  
 SLR : 245 QSRGGWLAVLALGATFLALCYFWWLPQLKFWQRWSLPLAIAVAVILGGGALIAVEPIRL 304  
  
 ICTB : 301 RVLSIFVGREDSNNFRINWVLAVLQMIQDRFWLIGIGPGNTAFNLVPLYQQARFTALSA 360  
 R +SIF GREDSNNFRINWV V MI+ RP +GIGPGN AFN +YP Y + RFTALSA  
 SLR : 305 RAMSIFAGREDSNNFRINWVEGVKAMIRARPIIGIGPGNEAFNQIYPYMRPRFTALSA 364  
  
 ICTB : 361 YSVPLEVAVEGGLGLTAFWLLLVTAVTAVRQVSRLRRDRNPQAFWLMASLAGLMLG 420  
 YS+ LE+ VE G++G T WLL VT V V R R+ P+ W+M +LA + G+L  
 SLR : 365 YSIYLEILVETGVGFTCMLWLLAVTLGKGVLEVVKRCRQTLAPEGIWMGALAAIIGLLV 424  
  
 ICTB : 421 HGLFDTVLYRPEASTLWLCIGAIASFHQPSKQLPPEAEHSDEKM 467  
 HG+ DTV YRP STLWNL + +AS W ++ + E+ D+ +  
 SLR : 425 HGMVDTVWYRPPVSTLWLLVAIVASQWASQAARLEASKEENEDKPL 471

Fig. 3

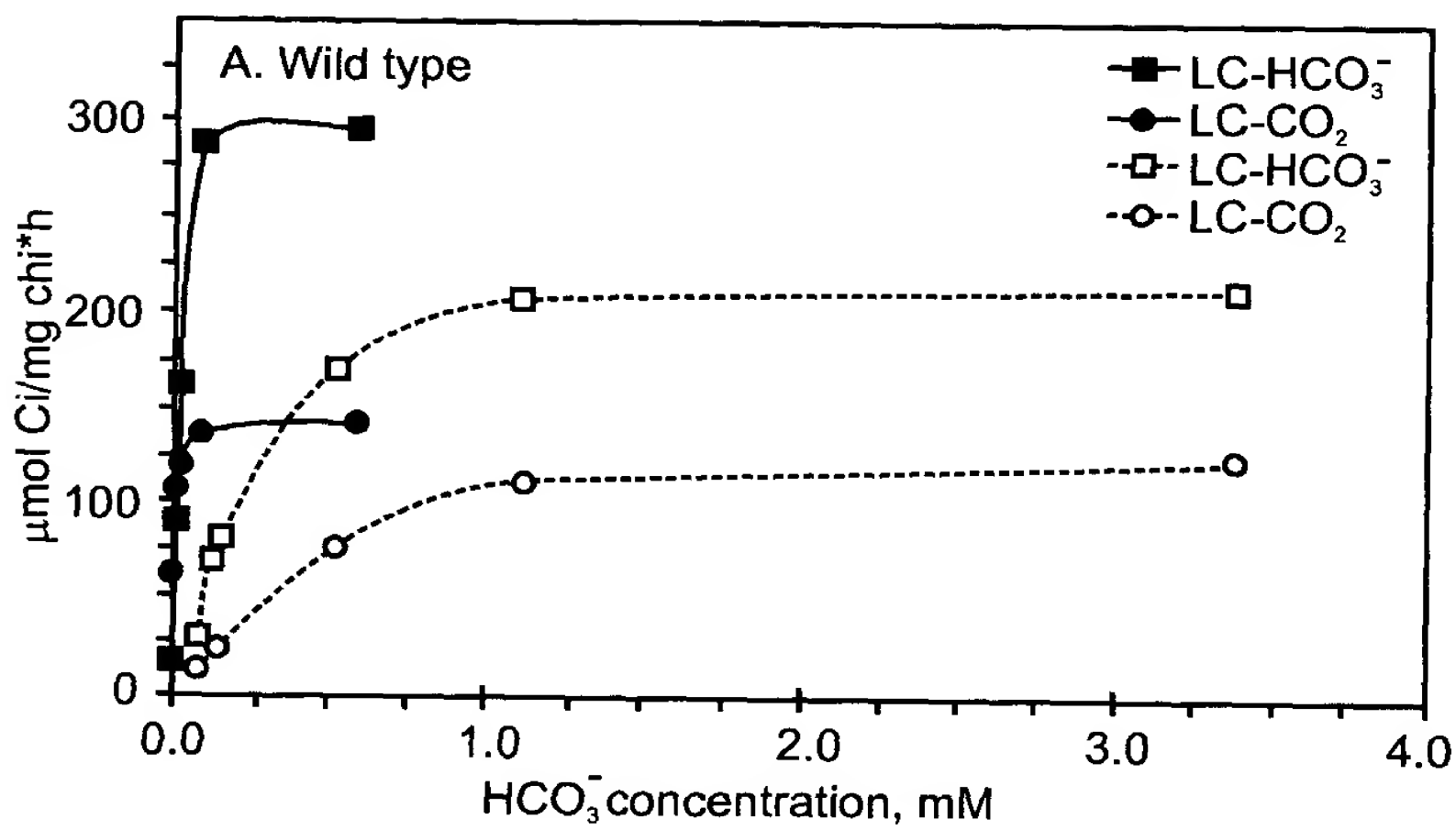


Fig. 4a

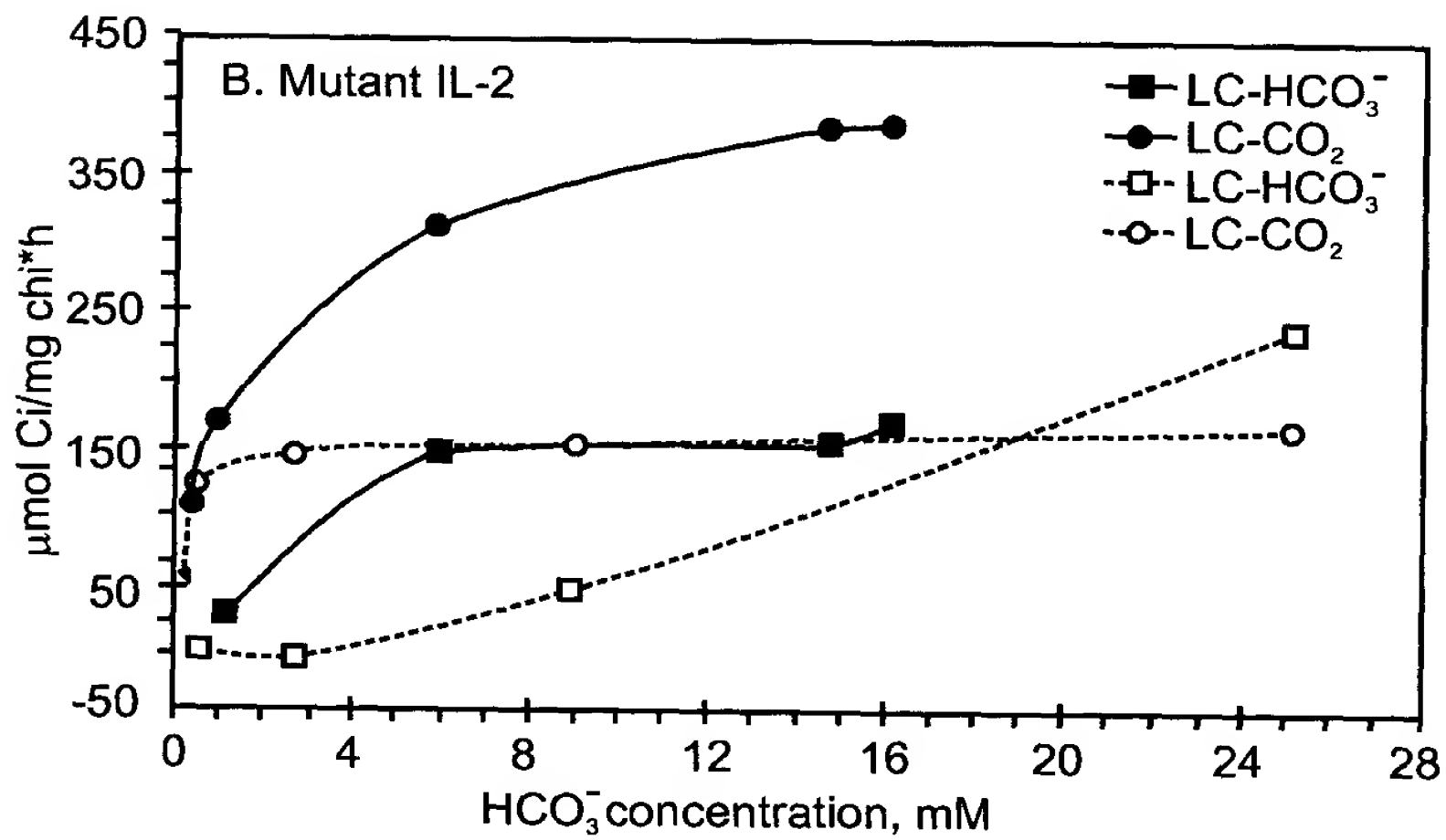


Fig. 4b

Wild type	GGGCT-AGCCGCGA	CGCGGCCCTATTGGGCCC	(SEQ ID NO: 6)
IL-2 ApaI side	GGGCT-AG--G-GATCGC	-GCCCTATTGGGCCC	(SEQ ID NO: 7)
IL-2 BamHI side	GGGCTCA-----GATCGC	-GCCCTATTGGGCCC	(SEQ ID NO: 8)
IctB	G L A A I A A Y W A L	(SEQ ID NO: 9)	

Fig. 5

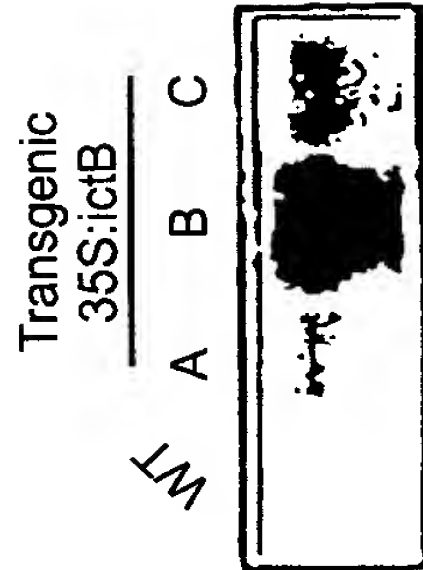


Fig. 6